



st99021seq1t.ST25
SEQUENCE LISTING

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<120> SYSTEM OR REGULATION OF EXPRESSION USING PPAR NUCLEAR RECEPTORS

<130> ST99021 US PCT

<140> 10/018,729

<141> 2001-12-18

<150> FR 99/07957

<151> 1999-06-22

<150> US 60/149,721

<151> 1999-08-20

<150> PCT/FR00/01744

<151> 2000-06-22

<160> 28

<170> PatentIn version 3.0

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<212> DNA

<213> Artificial

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<223> sequence of a site in the PPAR response element

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tcaaccttta ccctggtag

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<212> PRT
<213> Homo sapiens

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Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser

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Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val	20	25	30
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	35	40	45
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro	50	55	60
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp	65	70	75
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp	85	90	95
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser	100	105	110
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu	115	120	125
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp	130	135	140
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys	145	150	155
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys	165	170	175
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr	180	185	190
Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile	195	200	205
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu	210	215	220
Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg	225	230	235
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu	245	250	255
Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys	260	265	270
Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp	275	280	285
Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu	290	295	300
Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala	305	310	315
Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn	325	330	335
Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu			

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340		345		350
Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu	355	360	365	
Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu	370	375	380	
Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val	385	390	395	400
Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile	405	410		415
Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys	420	425		430
Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln	435	440	445	
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu	450	455	460	
Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu	465	470	475	480
Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu	485	490		495
Leu Gln Glu Ile Tyr Lys Asp Leu Tyr Ala Trp Ala Ile Leu Thr Gly	500	505		510
Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu	515	520	525	
Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln	530	535	540	
Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe	545	550	555	560
Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile	565	570		575
Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys	580	585	590	
Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn	595	600	605	
Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu	610	615	620	
Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys	625	630	635	640
Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp	645	650		655
Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly	660	665	670	
Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln				

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675		680		685
Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu				
690		695		700
Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr				
705		710		720
Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met				
	725		730	735
Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr				
	740		745	750

<210> 25
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 <213> Homo sapiens

<400> 25

Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln				
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Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe				
	20		25	30
Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile				
	35		40	45
Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys				
	50		55	60
Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn				
65		70		75
Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu				
	85		90	95
Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys				
	100		105	110
Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp				
	115		120	125
Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly				
	130		135	140
Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln				
145		150		155
Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu				
	165		170	175
Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr				
	180		185	190
Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met				
	195		200	205
Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr Ala Trp				
	210		215	220

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Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr
225 230 235 240

Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His
245 250 255

Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe
260 265 270

Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu
275 280 285

Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln
290 295 300

Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu
305 310 315 320

Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly
325 330 335

Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp
340 345 350

Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu
355 360 365

Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser
370 375 380

Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln
385 390 395 400

Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro
405 410 415

Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu
420 425 430

Arg Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys
435 440 445

Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys
450 455 460

Asp Leu Tyr
465

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cccgttacat aacttacggt aaatggcccg

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st99021seq1t.ST25

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gggacgcgct tctacaaggc gctggccgaa

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<210> 28

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cgactctaga agatcttgcc ccgcccagcg

30